METHODS FOR IDENTIFYING SUBJECTS SUSCEPTIBLE TO ATAXIC NEUROLOGICAL DISEASE

GOVERNMENT RIGHTS

The present invention was made with government support under Contract No: VISN 20 MIRECC awarded by the Department of Veterans Affairs. The United States government has certain rights in the invention.

CROSS-REFERENCE TO RELATED APPLICATION

This application claims the benefit of U.S. Provisional Application No. 60/414,816, filed September 26, 2002.

FIELD OF THE INVENTION

The present application relates to methods and kits for identifying subjects susceptible to ataxia.

BACKGROUND OF THE INVENTION

The nonepisodic, autosomal dominant, spinocerebellar ataxias (SCA) share the clinical features of progressive incoordination of gait, hand and eye movements and dysarthria, associated with degeneration of the cerebellar cortex and other regions of the central nervous system. Additional features, such as mental retardation, retinopathy, sensory neuropathy or myoclonus are found in some members of the disease family. The incidence of the disease is approximately 1 to 5/100,000, with an average age of onset in the third decade.

There are at least 20 genetically distinct autosomal dominant SCAs (see Mariotti, C., DiDonato, S., "Cerebellar/spinocerebellar syndromes," *Neurol. Sci. 22*:S88-S92 (2001)). Trinucleotide repeat expansions $(CAG)_n$, coding for polyglutamine tracts are responsible for SCA1,SCA2,SCA3,SCA6,SCA7, SCA12 and SCA17, whereas expanded

CTG and ATTCT repeats are responsible for SCA8 and SCA10, respectively. In North American populations approximately 30% of SCA families are not linked to the known loci (Moseley et al., *Neurology 51*:1666-1671, 1998).

Given the prevalence of SCA cases not linked to any known genetic loci, there is a need to identify genetic mutations associated with the SCA syndromes that can be used in a genetic screen to identify subjects susceptible to ataxic neurological disease. The present inventors have discovered that individuals with mutations in the protein kinase C gamma ("PRKCG") gene, coding for the protein kinase C gamma protein ("PKCγ"), display an adult onset ataxia.

SUMMARY OF THE INVENTION

In accordance with the foregoing, in one aspect the present invention provides methods of identifying genetic mutations that are associated with ataxic neurological disease in a mammalian subject, the methods comprising identifying a difference between a nucleic acid sequence of a protein kinase C gamma gene from a first mammalian subject exhibiting ataxia and a nucleic acid sequence of a protein kinase C gamma gene from a second mammalian subject which is not exhibiting ataxia, wherein the first and second mammalian subjects are members of the same species, and wherein the difference between the nucleic acid sequences is a genetic mutation that is associated with ataxic neurological disease. In some embodiments of this aspect of the invention, the method further comprises determining whether the identified mutations cosegregate with ataxia.

In another aspect, the present invention provides an isolated nucleic acid molecule encoding a protein kinase C gamma protein comprising a missense mutation selected from the group consisting of R41P, H101Y, S119P, Q127R, G128D, S361G and R597S.

In another aspect, the present invention provides methods of screening a mammalian subject to determine if said subject has a genetic predisposition to develop an ataxic neurological disease, or is suffering from an ataxic neurological disease. The method of this aspect of the invention comprises analyzing the nucleic acid sequence of a protein kinase C gamma gene in a mammalian subject to determine whether a genetic mutation that is associated with an ataxic neurological disease is present in the nucleic acid sequence, wherein the presence of a genetic mutation in the protein kinase C gamma gene that cosegregates with an ataxic neurological disease indicates that the mammalian

subject has a genetic predisposition to develop an ataxic neurological disease or is suffering from an ataxic neurological disease.

In another aspect, the invention provides a kit for determining susceptibility or presence of ataxic neurological disease, said kit comprising (i) one or more nucleic acid primer molecules for amplification of a portion of the protein kinase C gamma gene and (ii) written indicia indicating a correlation between the presence of said mutation and risk of ataxic neurological disease. In some embodiments, the kit further comprises means for determining whether a mutation associated with ataxic neurological disease is present. In some embodiments, the kit detects the presence or absence of a mutation in the protein kinase C gamma gene selected from the group consisting of R41P, H101Y, S119P, Q127R, G128D, S361G and R597S.

The invention thus provides methods and kits for identifying genetic mutations in a protein kinase C gamma gene and thereby facilitates diagnosis of ataxic neurological disease and identification of carriers of the genetic defect. The nucleic acid molecules of the invention are useful for as probes to identify genetic mutations in the protein kinase C gamma gene and have therapeutic utility for identifying compounds that can be used to treat ataxic neurological disease.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

Unless specifically defined herein, all terms used herein have the same meaning as they would to one skilled in the art of the present invention. Practitioners are particularly directed to Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Press, Plainsview, New York, and Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York (1999) for definitions and terms of art.

The following definitions are provided in order to provide clarity with respect to the terms as they are used in the specification and claims to describe the present invention.

As used herein, the term "ataxia" refers to poor coordination of movement and a wide-based, uncoordinated, unsteady gait. Ataxia may result, for example, from dysfunction of the cerebellum and its associated systems, lesions in the spinal cord, peripheral sensory loss, or any combination of these conditions.

As used herein, the term "myoclonus" refers to sudden brief involuntary movements of a muscle or limb.

As used herein, the term "cerebellum" refers to the portion of the brain lying at the back of the skull that is particularly involved with the coordination of movement.

As used herein, the term "nystagmus" refers to involuntary jerky eye movements.

As used herein, the term "dysarthria" refers to difficulty in articulating words.

As used herein, the term "ataxic neurological disease" refers to the clinical manifestation of a slowly progressive incoordination of gait and poor coordination of hand and eye movements which may also be associated with degeneration of the cerebellar cortex and spinal pathways.

As used herein, the term "primer" means a polynucleotide generally having a length of 5 to 50 nucleotides which can serve to initiate a nucleic acid chain extension reaction.

As used herein, the term "protein kinase C gamma (PRKCG) gene" refers to any gene that encodes the PRKCG protein. Some PRKCG genes useful in the practice of this invention are at least 90% identical to the nucleic acid sequence set forth in SEQ ID NO:3. Some PRKCG genes useful in the practice of this invention are at least 95%, or at least 99% identical to the nucleic acid sequence set forth in SEQ ID NO:3.

As used herein, the term "sequence identity" or "percent identical" as applied to nucleic acid molecules is the percentage of nucleic acid residues in a candidate nucleic acid molecule sequence that are identical with a subject nucleic acid molecule sequence (such as the nucleic acid molecule sequence set forth in SEQ ID NO:3), after aligning the sequences to achieve the maximum percent identity, and not considering any nucleic acid residue substitutions as part of the sequence identity. No gaps are introduced into the candidate nucleic acid sequence in order to achieve the best alignment. Nucleic acid sequence identity can be determined in the following manner. The subject polynucleotide molecule sequence is used to search a nucleic acid sequence database, such as the Genbank database, using the program BLASTN version 2.1 (based on Altschul et al., *Nucleic Acids Research 25*:3389-3402 (1997)). The program is used in the ungapped mode. Default filtering is used to remove sequence homologies due to regions of low complexity as defined in Wootton, J.C. and S. Federhen, *Methods in Enzymology 266*:554-571 (1996). The default parameters of BLASTN are utilized.

As used herein, the term "genetic mutation" is an alteration of the wild-type protein kinase C gamma (PRKCG) sequence deposited in GenBank, provided as SEQ ID NO:3 that is not a recognized polymorphism (i.e., has a population frequency less than 1% in mammalian control subjects of the same species that do not exhibit ataxia).

In one aspect, the present invention provides methods of identifying genetic mutations that are associated with ataxic neurological disease in a mammalian subject. The methods of this aspect of the invention comprise the step of identifying a difference between a nucleic acid sequence of a protein kinase C ("PRKCG") gene from a first mammalian subject exhibiting ataxia and a nucleic acid sequence of a PRKCG gene from a second mammalian subject which is not exhibiting ataxia, wherein the first and second mammalian subjects are members of the same species, and wherein the difference between the nucleic acid sequences is a genetic mutation that is associated with ataxic neurological disease. In some embodiments, the method further comprises the step of determining whether the identified genetic mutation cosegregates with ataxia.

The methods of this aspect of the invention are useful to identify genetic mutations associated with ataxic neurological disease in any mammalian subject, particularly human subjects. For example, the methods of the invention may be used to identify genetic mutations in the PRKCG gene that are associated (i.e., where the mutation is found to occur in subjects predisposed to develop ataxic neurological disease and the mutation is not found in subjects not predisposed to develop ataxic neurological disease) with the occurrence of ataxic neurological disease in individuals at risk for developing this disease.

The present inventors have discovered that mutations in the PRKCG gene locus are responsible for a portion of cases of ataxic neurological disease not attributed to SCA1,2,3 and 6. PRKCG was identified as a candidate gene based in part on chromosomal mapping to a 22 cM region on chromosome 19q13.4-qter as described in Example 1. PKCγ is a member of the conventional subgroup (cPKC) of a serine/threonine kinase family (Coussens et al., *Science 233*:859-866 (1986); Knopf et al., *Cell 46*:491-502 (1986)) that plays a role in such diverse processes as signal transduction, cell proliferation and differentiation, synaptic transmission and tumor promotion (see Tanaka and Nishizuka, *Annu. Rev. Neurosci. 17*:551-567 (1994)).

The amino-terminal regulatory domain of PKCγ contains two cysteine-rich regions (cys1 and cys2), collectively termed C1, each of which interacts with two zinc ions and provides high affinity diacylglycerol (DAG)/phorbol ester binding, and a Ca^{2+} sensitive region (C2) (reviewed in Newton A.C., *Chem. Rev. 101*:2353-2364 (2001)). The carboxyl-terminal catalytic domain contains kinase and substrate recognition regions.

The PRKCG human gene encompasses 24 kilobases and consists of 18 exons. The PRKCG cDNA coding sequence is provided herein as SEQ ID NO:1 which corresponds to nucleotides 187-2280 of GenBank accession number NM_002739. Disclosed herein are nucleic acid mutations numbered sequentially with respect to the first nucleotide of SEQ ID NO:1. The PKCγ protein encoded by SEQ ID NO:1 is provided herein as SEQ ID NO:2. Disclosed herein are amino acid mutations numbered sequentially with respect to the first amino acid residue of SEQ ID NO:2. The entire 25 kilobase genomic locus that encompasses the PRKCG gene is provided herein as SEQ ID NO:3. With respect to the first nucleotide in SEQ ID NO:3, the 18 exons are as follows: exon 1: nucleotides 440 to 609; exon 2: nucleotides 1108 to 1139; exon 3: 2106 to 2188; exon 4: nucleotides 7583 to 7694; exon 5: nucleotides 7831 to 7962; exon 6: nucleotides 9619 to 9775; exon 7: nucleotides 10454 to 10588; exon 8: nucleotides 10933 to 11020; exon 9: nucleotides 11307 to 11336; exon 10: nucleotides 15904 to 16056; exon 11: nucleotides 16385 to 16573; exon 12: nucleotides 18178 to 18269; exon 13: nucleotides 18364 to 18426; exon 14: nucleotides 18556 to 18694; exon 15: nucleotides 21018 to 21098; exon 16: nucleotides 22580 to 22687; exon 17: nucleotides 24262 to 24402; and exon 18: nucleotides 24652 to 24840.

The present inventors have identified several missense mutations (for example, H101Y, S119P, and G128D) in the Cys2 region of the C1 domain of PKCγ (SEQ ID NO:2) that cause a disease that is clinically indistinguishable from other "uncomplicated" SCAs (see Example 1, Example 2 and Chen et al., *Am. J. Hum. Genet. 72*:839-849, 2003, incorporated herein by reference). The patients with mutations in PRKCG (as described in Examples 1 and 2) displayed an adult-onset cerebellar ataxia without any differentiating features such as cognitive decline, visual or other sensory loss, axial myoclonus or peripheral neuropathy. The practice of this aspect of the invention is therefore useful to identify additional mutations in the PRKCG gene that are associated with ataxic neurological disease.

In the practice of this aspect of the method of the invention, any method of obtaining reliable nucleic acid sequence data from a mammalian subject exhibiting ataxia may be utilized. For example, reliable sequence data may be obtained from existing databases of sequence data, or alternatively, a reliable nucleic acid assay that will identify a genetic mutation in the PRKCG may be utilized.

In one embodiment of the methods of the invention, a genetic mutation is detected by amplification of all or part of the PRKCG gene from genomic DNA followed by sequencing of the amplified DNA. For example, each of the 18 exons of the PRKCG gene may be amplified individually or in combination using as template genomic DNA from a test subject exhibiting ataxia. A method of amplification which is well known by those skilled in the art is the polymerase chain reaction (PCR) (see *Current Protocols in Molecular Biology*, Ausubel, F.M. et al., John Wiley & Sons; 1995). Alternative amplification techniques may also be used in the method of this aspect of the invention, such as the ligase chain reaction (LCR) (Wu and Wallace, *Genomics 4*:560-569 (1989)), strand displacement amplification (SDA) (Walker et al., *Proc. Nat'l. Acad. Sci. USA 89*:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al., *PCR Methods Appl. 1*:25-33 (1992)), and Branched Chain Amplification which are known and available to persons skilled in the art.

The PCR process involves the use of pairs of primers, one for each complementary strand of the duplex DNA (wherein the coding strand is referred to as the "sense strand" and its complementary strand is referred to as the "anti-sense strand"), that will hybridize at sites located on either side of a region of interest in a gene. Chain extension polymerization is then carried out in repetitive cycles to increase the number of copies of the region of interest exponentially. Primers useful in the practice of the method of the invention comprise polynucleotides that hybridize to a region of a PRKCG gene, which can serve to initiate a chain extension reaction. A "primer pair" is a pair of primers which specifically hybridize to sense (coding) and antisense (non-coding) strands of a duplex polynucleotide to permit amplification of the region lying between the primers of the pair. Primers useful in the practice of this aspect of the invention comprise a polynucleotide ranging from 5 to 50 bp of continuous sequence chosen from SEQ ID NO:1 or SEQ ID NO:3. For example, primer pairs suitable for PCR amplification and sequencing of each of the 18 exons in PRKCG are described in TABLE 1 and TABLE 2.

TABLE 1 describes SEQ ID NOS: 4-35 which are primers useful for amplification and sequencing the PRKCG gene in the practice of the method of the invention. The first column of TABLE 1 describes the SEQ ID NO, the second column provides the nucleotide sequence of the primer, and the third column provides the exon name given to the primer. TABLE 2 describes sets of primers useful for PCR amplifying the 18 exons of the PRKCG gene from genomic DNA. The first column of TABLE 2 describes the exon to be amplified, and the second and third columns provide the forward and reverse primers used to amplify the exon. Tm refers to the melting temperature of the oligonucleotide pair. The expected PCR product size in base pairs (bp) for each PCR amplification is provided in the fifth column. The right side of TABLE 2 provides a set of primers useful for sequencing across each exon. Example 1 provides a non-limiting example of this embodiment of the method of the invention.

In one embodiment of the method of the invention, after amplification, genetic mutations are detected in the amplified DNA by sequence analysis. Methods of DNA sequence analysis are well known in the art. A well known method of sequencing is the "chain termination" method first described by Sanger et al., *PNAS (USA) 74*(12):5463-5467 (1977) and detailed in SEQUENASE™ 2.0 product literature (Amersham Life Sciences, Cleveland). Sequencing can be performed using a single primer or a primer pair. Primers are chosen for sequencing based on their proximity to the region of interest. Non-limiting examples of suitable sequencing primers for each exon are described in TABLE 1 and TABLE 2.

TABLE 1

SEQ ID #	Oligo primer SEQ 5'-3'	Exon
4	ctgcctttggctcttcct	1F
5	taggagtctgcacccctagt	1R
6	ctggattcctgggtctgaag	2F
7	cagcctccaccctcctga	2R
8	cgctctctctttccaatttt	3F
9	gaggaggagaaccaggtgt	3R
10	caaggcaggaggaaaagata	4F
11	atttcccggaacccagac	4R

SEQ ID #	Oligo primer SEQ 5'-3'	Exon
12	catgaaatgctcctgtgagt	5F
13	acaagtgccttgggtcag	5R
14	gcttggaactcttgattgct	6F
15	ccactaggaccctcagatca	6R
16	acctccagcaccaaggat	7F
17	cacacacagatggagatggt	7R
18	cttccaatgtctttgcctct	8F
19	atgtgtggggaattgaagac	9R
20	ttgggagcatttccttatcg	10F
21	aaatctgaccttcccacaga	10R
22	tcccttaagagatggaggaa	11F
23	ctcgccctaaactcagaatc	11R
24	gtctgatagttggcggtggt	12F
25	agaaggtcagtggctggat	12R
26	atccagccactgaccttct	13F
27	cagtgccaagctcacctg	14R
28	gggaagagcttgtgctgaaa	15F
29	ctaactggctcctcctgaga	15R
30	ggcatccgagataggaaatg	16F
31	tcaggaatgggagcattttt	16R
32	ttctctgggtctacctgtcc	17F
33	gtgtctgcacctccttttgt	17R
34	cagacaccatgaagcatgaata	18F
35	ttagtggtgtggtctctgga	18R

TABLE 2

PRIMERS FOR EXON FRAGMENT AMPLIFICATION AND SEQUENCING OF PRKCG GENE

PCR AMPLIFICATION						SEQUENCING REACTION		
Exon	*Forward*	*Reverse*	*Tm*	*Size bp*		*Exon*	*Forward*	*Reverse*
1+2	1F (SEQ ID NO:4)	2R (SEQ ID NO:7)	62	1016		1	1F (SEQ ID NO:4)	1R (SEQ ID NO:5)
						2	2F (SEQ ID NO: 6)	2R (SEQ ID NO:7)
3	3F (SEQ ID NO:8)	3R (SEQ ID NO:9)	56	203		3	3F (SEQ ID NO:8)	3R (SEQ ID NO:9)
4+5	4F (SEQ ID NO:10)	5R (SEQ ID NO:13)	60	542		4	4F (SEQ ID NO:10)	4R (SEQ ID NO:11)
						5	5F (SEQ ID NO:12)	5R (SEQ ID NO:13)
6	6F (SEQ ID NO:14)	6R (SEQ ID NO:15)	56	310		6	6F (SEQ ID NO:14)	6R (SEQ ID NO:15)
7+8+9	7F (SEQ ID NO:16)	9R (SEQ ID NO:19)	60	1059		7	7F (SEQ ID NO:16)	7R (SEQ ID NO:17)
						8+9	8F (SEQ ID NO:18)	9R (SEQ ID NO:19)
10+11	10F (SEQ ID NO:20)	11R (SEQ ID NO:23)	56	825		10	10F (SEQ ID NO:20)	10R (SEQ ID NO:21)
						11	11F (SEQ ID NO:22)	11R (SEQ ID NO:23)
12+13+14	12F (SEQ ID NO:24)	14R (SEQ ID NO:27)	60	896		12	12F (SEQ ID NO:24)	12R (SEQ ID NO:25)
						13+14	13F (SEQ ID NO:26)	14R (SEQ ID NO:27)
15+16	15F (SEQ ID NO:28)	16R (SEQ ID NO:31)	56	1880		15	15F (SEQ ID NO:28)	15R (SEQ ID NO:29)
						16	16F (SEQ ID NO:30)	16R (SEQ ID NO:31)
17+18	17F (SEQ ID NO:32)	18R (SEQ ID NO:35)	56	932		17	17F (SEQ ID NO:32)	17R (SEQ ID NO:33)
						18	18F (SEQ ID NO:34)	18R (SEQ ID NO:35)

Once the nucleic acid sequence from the test subject is obtained, the sequence is compared to the nucleic acid sequence of one or more subjects not exhibiting ataxia in order to identify genetic mutations that are associated with ataxia. For example, resulting sequences can be aligned with the known exon sequence using a multiple sequence alignment tool, Sequencher (Gene Codes Corporation, Ann Arbor, MI), in order to identify any nucleotide changes as described in Example 4. In one embodiment, the information and analysis can be recorded on a database and the comparisons can be performed by a computer system accessing said database. In this manner, the amplified sequences of PRKCG from a subject exhibiting ataxia are sequenced until a mutation associated with ataxia is identified.

A mutation associated with ataxia encompasses any alteration of the wild-type protein kinase C gamma (PRKCG) sequence deposited in GenBank, provided as SEQ ID NO:3, that is not a recognized polymorphism (i.e., has a population frequency less than 1% in mammalian control subjects of the same species that do not exhibit ataxia). A genetic mutation may be any form of sequence alteration including a deletion, insertion, point mutation or DNA rearrangement in the coding or noncoding regions. Deletions may be small or large and may be of the entire gene or of only a portion of the gene. Point mutations may result in stop codons, frameshift mutations or amino acid substitutions. Point mutations may also occur in regulatory regions, such as in the promoter of the PRKCG gene, leading to loss or diminution of expression of the mRNA. Point mutations may also abolish proper RNA processing, leading to loss of expression of the PRKCG gene product, or to a decrease in mRNA stability or translation efficiency. DNA rearrangements include a simple inversion of a single segment of DNA, a reciprocal or nonreciprocal translocation disrupting any portion of the gene, or a more complex rearrangement. The following characteristics are supportive, but are not required for a genetic mutation to be a causative mutation for ataxic neurological disease: 1) the change results in an amino acid substitution in a highly evolutionarily conserved residue; 2) the change occurs in a functional domain; 3) the change is predicted to affect splicing; or 4) the change cosegregates with disease in a family (where applicable).

In one embodiment of this aspect of the method of the invention, once a mutation is identified in a subject exhibiting ataxia, co-segregation analysis is carried out to determine if the particular mutation in the PRKCG gene co-segregates with the presence

of ataxic neurological disease symptoms in the subjects tested. Co-segregation analysis can be done in several ways. In one embodiment, co-segregation analysis is done by sequencing DNA amplified from the corresponding exon in subjects exhibiting ataxia utilizing the previously described methods. For example, DNA sequence variations can be identified using DNA sequencing, as described in Example 1. Alternatively, there are several other methods that can be used to detect and confirm DNA sequence variation including, for example, (1) single stranded conformation analysis (SSCA)(Orita et al., *Proc. Nat'l. Acad. Sci. USA 86*:2776-2770 (1989)); (2) denaturing gradient gel electrophoresis (DGGE) based on the detection of mismatches between the two complementary DNA strands (Wartell et al., *Nucl. Acids Res. 18*: 2699-2705 (1990)); (3) RNase protection assays (Finkelstein et al., *Genomics 7*:167-172 (1990)); (4) hybridization with allele-specific oligonucleotides (ASOs)(Conner et al., *Proc. Nat'l. Acad. Sci. USA 80*:278-282 (1983)) and (5) allele-specific PCR (Rano & Kidd, Nucl. *Acids Res. 17*:8392 (1989)). In the SSCA, DGGE and RNase protection assay, a new electrophoretic band appears when a mutation is present. SSCA detects a band which migrates differently because the sequence change causes a difference in single-strand, intramolecular base pairing. DGGE detects differences in migration rates of mutant sequences compared to wild-type sequences using a denaturing gradient gel. For allele-specific PCR, primers are used which hybridize at their 3' ends to a particular PRKCG mutation. If the particular PRKCG mutation is not present, an amplification product is not observed. Insertions and deletions of genes can also be detected by cloning, sequencing and amplification.

In another embodiment, genetic mutations are identified by hybridization of amplified regions of the PRKCG gene with allele-specific oligonucleotides. For example, a hybridization assay may be carried out by isolating genomic DNA from a mammalian subject exhibiting ataxia, hybridizing a DNA probe onto said isolated genomic DNA, said DNA probe spanning said mutation in said gene, wherein said DNA probe is capable of detecting said mutation; treating said genomic DNA to determine the presence or absence of said DNA probe and thereby indicating the presence or absence of said genetic mutation. Desirable probes useful in such a DNA hybridization assay comprise a nucleic acid sequence that is unique to the genetic mutation. Analysis can involve denaturing gradient gel electrophoresis or denaturing HPLC methods, for

example. For guidance regarding probe design and denaturing gel eletrophoresis or denaturing HPLC methods, see, e.g., Ausubel et al., 1989, *Current Protocols in Molecular Biology*, Green Publishing Associates and Wiley Interscience, N.Y.

In another embodiment of this aspect of the method of the invention, restriction fragment length polymorphism (RFLP) for the gene can be used to score for a genetic mutation in a co-segregation analysis. RFLP has been described in U.S. Patent Nos. 4,965,188; 4,800,159, incorporated herein by reference. In this technique, restriction enzymes are used which provide a characteristic pattern of restriction fragments, wherein a restriction site is either missing or an additional restriction site is introduced in the mutant allele. Thus, DNA from an individual and from control DNA sequences are isolated and subjected to cleavage by restriction enzymes which are known to provide restriction fragments which differentiate between normal and mutant alleles, and the restriction patterns are identified. Example 3 further illustrates RFLP methods that are useful in the practice of the method of the invention.

Several genetic mutations in PRKCG that are associated with ataxia have been identified by practicing the methods of this aspect of the invention as described in Examples 1-3 and shown in TABLE 3. TABLE 3 provides a list of mutations identified in a PRKCG gene using the methods of this aspect of the invention. The first column of TABLE 3 describes the exon the mutation resides in, the second column describes the nucleotide change in the cDNA (numbered sequentially with reference to SEQ ID NO:1) for each mutant, the third column describes the type of mutation that is present (missense, silent, deletion, etc.), the fourth column describes primer pairs useful to PCR amplify the exon containing the mutation and the fifth column describes primers useful for sequencing across the region containing the mutation.

In another aspect, the present invention provides isolated nucleic acid molecules encoding a protein kinase C gamma protein comprising a mutation selected from the group consisting of R41P, H101Y, S119P, Q127R, G128D, S361G and R597S. The mutations in the PKCγ protein are numbered sequentially with respect to the first amino acid of SEQ ID NO:2. The nucleotide sequences are numbered sequentially according to the first nucleotide of SEQ ID NO:1. Each mutation is further described as follows:

Mutation R41P results from a nucleotide change of G to C at nucleotide 122, which results in the codon change CGC to CCC which in turn results in the missense

mutation at amino acid R41 to P, substituting a proline for an arginine at amino acid residue 41.

Mutation H101Y results from a nucleotide change of C to T at nucleotide 301, which results in the codon change CAC to TAC which in turn results in the missense mutation at amino acid H101 to Y, substituting a tyrosine for a histidine at amino acid residue 101.

Mutation S119P results from a nucleotide change of T to C at nucleotide 355, which results in the codon change TCC to CCC which in turn results in the missense mutation at amino acid S119 to P, substituting a proline for a serine at amino acid residue 119.

Mutation Q127R results from a nucleotide change of A to G at nucleotide 380, which results in the codon change CAG to CGG which in turn results in the missense mutation at amino acid Q127 to R, substituting an arginine for a glutamine at amino acid residue 127.

Mutation G128D results from a nucleotide change of a G to A at nucleotide 383, which results in the codon change GGC to GAC which in turn results in the missense mutation at amino acid G128 to D, substituting an aspartic acid for a glycine at amino acid residue 128.

Mutation S361G results from a nucleotide change of an A to G at nucleotide 1081, which results in the codon change AGT to GGT which in turn results in the missense mutation at amino acid S361 to G, substituting a glycine for a serine at amino acid residue 361.

Mutation R597S results from a nucleotide change of a C to A at nucleotide 1789, which results in the codon change CGC to AGC which in turn results in the missense mutation at amino acid R597 to S, substituting a serine for an arginine at amino acid residue 597.

In this regard, in some embodiments the isolated nucleic acid molecules described herein are at least 90% identical to a portion of SEQ ID NO:1 or its complement. In some embodiments, the isolated nucleic acid molecules described herein are at least 90% identical to a portion of SEQ ID NO:3 or its complement. In some embodiments, the isolated nucleic acid molecules described herein hybridize to the complement of SEQ ID NO:1 under conditions of 5X SSC at 50°C for 1 hr. In some embodiments, the isolated

nucleic acid molecules described herein hybridize to the complement of SEQ ID NO:1 under conditions of 5X SSC at 60°C for 1 hr. In some embodiments, the isolated nucleic acid molecules described herein hybridize to the complement of SEQ ID NO:3 under conditions of 5X SSC at 50°C for 1 hr. In some embodiments, the isolated nucleic acid molecules described herein hybridize to the complement of SEQ ID NO:3 under conditions of 5X SSC at 60°C for 1 hr.

Some nucleic acid embodiments, for example, include genomic DNA, RNA and cDNA encoding the mutant proteins or fragments thereof. In some embodiments, the invention also encompasses DNA vectors such as, for example DNA expression vectors that contain any of the foregoing nucleic acid sequences operatively associated with a regulatory element that directs the expression of the coding sequences the nucleic acids above, and genetically engineered host cells that contain any of the foregoing nucleic acid sequences operatively associated with a regulatory element that directs the expression of the coding sequences in the host cell. The nucleic acids encoding the protein kinase C gamma protein mutations can be manipulated using conventional techniques in molecular biology so as to create recombinant constructs that express mutant polypeptides.

The nucleic acid sequences described above have diagnostic as well as therapeutic use. The nucleic acid sequences can be used as probes to identify more genetic mutations in the PRKCG gene and to detect the presence or absence of wild type or mutant genes in an individual, such as in nucleic acid hybridization assays, southern and northern blot analysis, and as controls for screening assays and the kits described herein. The sequences described herein can also be incorporated into constructs for preparing recombinant mutant proteins or used in methods of searching or identifying agents that modulate PRKCG levels and/or activity, for example, candidate therapeutic agents. Because the mutations of this aspect of the invention are dominant negative or gain of function mutations, they have also have therapeutic utility for use in the identification and development and design of drugs which circumvent or overcome the mutated PRKCG gene function. The sequences of the nucleic acids and/or proteins described herein can also be incorporated into computer systems and used with modeling software so as to enable rational drug design. Information from genotyping methods provided herein can be used, for example, in computer systems, in pharmacogenomic profiling of therapeutic

agents to predict effectiveness of an agent in treating an individual for an ataxic neurological disease.

The identification of mutant H101Y is described in Example 1. The identification of mutants R41P and S119P are described in Example 2. The identification of mutants Q127R, G128D, S361G and R597S are described in Example 4. The use of missense mutation H101Y to screen for ataxic neurological disease is further described in Example 1. The use of missense mutations S119P and G128D are further described in Example 2. The characterization of these mutations is described in TABLE 3.

In another aspect, the present invention provides methods of screening a mammalian subject to determine if said subject has a genetic predisposition to develop an ataxic neurological disease, or is suffering from an ataxic neurological disease. The methods of this aspect of the invention comprise the step of analyzing the nucleic acid sequence of a PRKCG gene in a subject to determine whether a genetic mutation that is associated with an ataxic neurological disease is present in the nucleic acid sequence, wherein the presence of such a mutation indicates that the mammalian subject has a genetic predisposition to develop ataxic neurological disease or is diagnosed as suffering from such as disease. In some embodiments, the method further comprises determining whether the mammalian subject is exhibiting ataxia. The clinical examination of a mammalian subject for symptoms related to ataxia may be done either prior to, or after nucleic acid analysis of the test subject.

The method of this aspect of the invention is useful for screening any mammalian subject, such as for example, a human subject, for the genetic predisposition to develop ataxic neurological disease. The method is especially useful for screening and diagnosing presymptomatic at-risk family members for the presence or absence of mutations associated with the disease. The method is also useful for screening subjects exhibiting ataxia to determine whether their symptoms are caused by a genetic mutation in the PRKCG gene.

Any genetic mutation in the PRKCG gene that cosegregates with an ataxic neurological disease is useful in the practice of the method of this aspect of the invention. Examples of such mutations are shown in TABLE 3.

TABLE 3
Mutations Identified in the PRKCG Gene

exon	nucleotide change in cDNA	Predicted amino acid change in protein	Type of mutation	Primers used to PCR amplify	Primers used to sequence
1	122G to C	R41P	missense	1F (SEQ ID NO:4); 2R (SEQ ID NO:7)	1F (SEQ ID NO:4); 1R (SEQ ID NO:5)
3	204C to G	V68V	silent *	3F (SEQ ID NO:8); 3R (SEQ ID NO:9)	3F (SEQ ID NO:8); 3R (SEQ ID NO:9)
3	207C to T	C69C	silent**	3F (SEQ ID NO:8); 3R (SEQ ID NO:9)	3F (SEQ ID NO:8); 3R (SEQ ID NO:9)
3	225A to G	R75R	silent *	3F (SEQ ID NO:8); 3R (SEQ ID NO:9)	3F (SEQ ID NO:8); 3R (SEQ ID NO:9)
3	285C to T (last nucleotide of exon 3)	D95D	silent, but alters the splice coefficient	3F (SEQ ID NO:8); 3R (SEQ ID NO:9)	3F (SEQ ID NO:8); 3R (SEQ ID NO:9)
4	296-301 del	del 100K, 101H	deletion	4F(SEQ ID NO: 10); 5R (SEQ ID NO:13)	4F(SEQ ID NO: 10); 4R (SEQ ID NO:11)
4	301C to T	H101Y	missense	4F(SEQ ID NO: 10); 5R (SEQ ID NO:13)	4F(SEQ ID NO: 10); 4R (SEQ ID NO:11)
4	355T to C	S119P	missense	4F(SEQ ID NO: 10); 5R (SEQ ID NO:13)	4F(SEQ ID NO: 10); 4R (SEQ ID NO:11)
4	380A to G	Q127R	missense	4F(SEQ ID NO: 10); 5R (SEQ ID NO:13)	4F(SEQ ID NO: 10); 4R (SEQ ID NO:11)
4	383G to A	G128D	missense	4F(SEQ ID NO: 10); 5R (SEQ ID NO:13)	4F(SEQ ID NO: 10); 4R (SEQ ID NO:11)
6	672T to C	N224N	silent**	6F (SEQ ID NO: 14); 6R (SEQ ID NO:15)	6F(SEQ ID NO: 14); 6R (SEQ ID NO:15)

exon	nucleotide change in cDNA	Predicted amino acid change in protein	Type of mutation	Primers used to PCR amplify	Primers used to sequence
10	1081A to G	S361G	missense	10F(SEQ ID NO: 20); 11R (SEQ ID NO:23)	10F(SEQ ID NO:20); 10R (SEQ ID NO:21)
12	1284C to T	D428D	silent*	12 (SEQ ID NO: 24); 14R (SEQ ID NO:27)	12F(SEQ ID NO: 24); 12R (SEQ ID NO:25)
16	1677C to T	D559D	silent*	15F(SEQ ID NO: 28); 16R (SEQ ID NO:31)	16F(SEQ ID NO: 30); 16R (SEQ ID NO: 31)
16	1683G to A	E561E	silent*	15F(SEQ ID NO:28); 16R (SEQ ID NO:31)	16F(SEQ ID NO: 30); 16R (SEQ ID NO: 31)
17	1789C to A	R597S	missense	17F(SEQ ID NO: 32); 18R (SEQ ID NO: 35)	17F(SEQ ID NO: 32); 17R (SEQ ID NO: 33)
* Silent mutations that have been detected in only one affected person and have not been observed in any of more than 200 other individuals					
**Silent mutations that have been detected in more than one affected person but have not previously been reported in the database as a polymorphism					

In one embodiment, genetic mutations that cosegregate with an ataxic neurological disease are missense mutations in which a nucleic acid base change results in an amino acid substitution in the PRKCG protein. Examples of such missense mutations include, for example, R41P, H101Y, S119P, Q127R, G128D, S361G, and R597S as shown in TABLE 3.

In another embodiment, the method of this aspect of the invention can be practiced using mutations that cause deletions, such as, for example, the deletion mutation identified in exon 4, shown in TABLE 3 which deletes nucleotides 296-301. Silent mutations which do not alter the amino acid sequence, but change splicing or gene regulation may also be used, such as for example, the mutation in exon 3 shown in TABLE 4 which changes nucleotide 285C to T, thereby altering the splicing coefficient of the PRKCG mRNA.

In some embodiments of the method of this aspect of the invention, subjects are screened for genetic mutations at one or more of the protein positions: 41, 101, 119, 127, 128, 361 or 597.

In some embodiments of this aspect of the method of the invention, subjects are screened for the presence of a genetic mutation that is associated with an ataxic neurological disease in exon 4 of a PRKCG gene, such as, for example, nucleotides 7583 to 7694 of SEQ ID NO: 3. Exon 4 encodes a region of highly conserved amino acid residues in the cys2 region of PRKCG gene. Examples of mutations found in exon 4 that cosegregate with ataxic neurological disease are shown in TABLE 3 and include H101Y, S199P, G128D, and Q127R.

Individuals carrying particular mutations in the PRKCG gene may be identified using a variety of techniques of analyzing nucleic acid sequence that are well known in the art such as, for example, direct sequencing, PCR amplification and sequencing, restriction fragment length polymorphism (RFLP), nucleic acid hybridization, and single strand conformation polymorphism (SSCP). For each of these techniques, the test subject provides a biological sample containing genomic DNA to be analyzed. The test sample may be obtained from body cells, such as those present in peripheral blood, urine, saliva, surgical specimen, and autopsy specimens. The test sample can be processed to inactivate interfering compounds, and to purify or partially purify the nucleic acids in the sample. Any suitable purification method can be employed to obtain purified or partially purified nucleic acids from the test sample. A lysing reagent optionally can be added to the sample, particularly when the nucleic acids in the sample are sequestered or enveloped, for example, by cellular or nuclear membranes. Additionally, any combination of additives, such as buffering reagents, suitable proteases, protease inhibitors, nucleases, nuclease inhibitors and detergents can be added to the sample to improve the amplification and/or detection of the nucleic acids in the sample. Additionally, when the nucleic acids in the sample are purified or partially purified, the use of precipitation can be used, or solid support binding reagents can be added to or contacted to the sample, or other methods and/or reagents can be used. One of ordinary skill in the art can routinely select and use additives for, and methods for preparation of a nucleic acid sample for amplification.

In one embodiment of the method of the invention, the nucleic acid sequence is analyzed by direct sequencing for differences in nucleic acid sequence from the wild-type PRKCG gene by sequencing of the subject's PRKCG gene using primers specific for the region of interest, such as, for example, the sequencing primers described in TABLE 1 and TABLE 2.

In another embodiment, prior to sequencing the DNA is amplified enzymatically in vitro through use of PCR (Saiki et al., *Science 239*:487-491 (1988)) or other in vitro amplification methods as previously described herein. In a further embodiment, the DNA from an individual can be evaluated using RFLP techniques are described in Example 3 and elsewhere herein. The previously described methods useful for determining co-segregation analysis are also useful in this aspect of the method of the invention, such as, for example, nucleic acid hybridization techniques and single strand conformation polymorphism (SSCP). SSCP is a rapid and sensitive assay for nucleotide alterations, including point mutations (see Orita, M., et al., *Genomics 5*:874-879 (1989). DNA segments ranging in length from approximately 100 bp to approximately 400 bp are amplified by PCR, heat denatured and electrophoresed on high resolution-non-denaturing gels. Under these conditions, each single-stranded DNA fragment assumes a secondary structure determined in part by its nucleotide sequence. Even single base changes can significantly affect the electrophoretic mobility of the PCR product.

In another aspect, the present invention provides kits for determining susceptibility or presence of ataxic neurological disease in a subject. The kits of the invention include (i) one or more nucleic acid primer molecules for amplification of a portion of the PRKCG gene, and (ii) written indicia indicating a correlation between the presence of said mutation and risk of ataxic neurological disease. In one embodiment, the kits of the invention further comprise means for determining whether a mutation associated with ataxic neurological disease is present. In some embodiments, the kits of the invention comprise detection components specific for one or more of the particular genetic mutations described herein.

Primer molecules for amplification of a portion of the PRKCG gene can be of any suitable length and composition and are selected to facilitate amplification of at least one or more regions (in the case of duplexed or multiplexed amplification) of the PRKCG as shown in SEQ ID NO: 3 that potentially contains a genetic mutation. For example,

oligonucleotide primers can be in the range of 5 bp to 50 bp or longer, and are chosen as primer pairs so that primers hybridize to sequences flanking the putative mutation. Primer pairs typically have an annealing temperature within about 20°C of each other. Computer programs are useful in the design of primers with the required specificity and optimal amplification properties. See, e.g., Oligo version 5.0 (available from National Biosciences Inc., 3001 Harbor Lane, Suite 156, Plymouth MN). Examples of primer pairs suitable for inclusion in the kit of the invention are provided in TABLE 2.

Similarly, a kit of the invention can also provide reagents for a duplexed amplification reaction (with two pairs of primers) a multiplexed amplification reaction (with three or more pair of primers) so as to amplify multiple sites of PRKCG nucleotide mutations in one reaction.

Also included in the kit of the invention are written indicia indicating a correlation (typically a positive correlation) between the presence of a particular mutation in the PRKCG gene and the risk of ataxic neurological disease.

The kit optionally also comprises one or more enzymes useful in the amplification or detection of nucleic acids and/or nucleotide sequences. Suitable enzymes include DNA polymerases, RNA polymerases, ligases, and phage replicases. Additional suitable enzymes include kinases, phosphatases, endonucleases, exonucleases, RNAses specific for particular forms of nucleic acids (including, but not limited to, RNAse H), and ribozymes. Other suitable enzymes can also be included in the kit.

The kit optionally comprises amplification reaction reagents suitable for use in nucleic acid amplification. Such reagents are well know and include, but are not limited to: enzyme cofactors such as magnesium or manganese; salts; nicotinamide adenine dinucleotide (NAD), and deoxynucleoside triphosphates (dNTPs). The kit optionally can also comprise detection reaction reagents, such as light or fluorescence generating substrates for enzymes linked to probes.

The kit optionally includes control DNA, such as positive and negative control samples. Negative control samples may comprise for example, genomic DNA or PRKCG cDNA from a mammalian subject with no predisposition to ataxic neurological disease, or portions thereof. Positive control samples may comprise, for example, nucleic acid molecules containing an identified mutation in the PRKCG gene as described herein.

The kit optionally includes instructions for using the kit in the detection of mutations in PRKCG associated with ataxic neurological disease. The kit also preferably includes instructions on the appropriate parameters for the amplification reaction. Any suitable set of amplification parameters can be employed. For example, the precise temperature at which double-stranded nucleic acid sequences dissociate, primers hybridize or dissociate, and polymerase is active, are dependent on the length and composition of the sequences involved, the salt content of the reaction, the oligonucleotide concentration, the viscosity of the reaction and the type of polymerase. One of ordinary skill in the art can easily determine appropriate temperatures for the amplification reaction (see, e.g., Wetmur, *J. Critical Reviews in Biochemistry and Molecular Biology 26:*227-59 (1991). For example, temperatures above about 90°C, such as between about 92°C, and about 100°C, are typically suitable for the dissociation of double-stranded nucleic acid sequences. Temperatures for forming primer hybrids are preferably between about 45°C and about 65°C. Temperatures for the polymerization/extension phase are typically between about 60°C and about 90°C, depending on the polymerase utilized in the reaction.

A multiplicity of suitable methods may be used to analyze the amplified nucleic acid product to determine whether a mutation associated with ataxic neurological disease is present. Suitable means include DNA sequencing, northern blotting, southern blotting, Southwestern blotting, probe shift assays (see, e.g., Kumar et al., *AIDS Res. Hum. Retroviruses 5:*345-54 (1989), T4 Endonuclease VII-mediated mismatch-cleavage detection (see, e.g., Youil et al., *Proc. Nat'l. Acad. Sci. USA 92:*87-91 (1995)), Fluorescence Polarization Extension (FPE), Single Strand Length Polymorphism (SSLP), PCR-Restriction Fragment Length Polymorphism (PCR-RFLP), Immobilized Mismatch Binding Protein Mediated (MutS-mediated) Mismatch detection (see, e.g., Wagner et al., *Nucleic Acids Research 23*:3944-48 (1995), reverse dot blotting, (see, e.g., European Patent Application No. 0 511 559), hybridization-mediated enzyme recognition (see, e.g., Kwiatkowski et al., *Mol. Diagn.*, *4*(4):353-64 (1999), describing the Invader™ embodiment of this technology by Third-Wave Technologies, Inc.), detection, single-strand conformation polymorphism (SSCP) and gradient denaturing gel electrophoresis to detect probe-target mismatches (e.g., "DGGE", see, e.g., Abrams et al., *Genomics 7*:463-

75 (1990), Ganguly et al., *Proc. Nat'l. Acad. Sci. USA 90*:10325-29 (1993), and Myers et al., *Methods Enzymology 155*:501-27 (1987)).

The kit is preferably provided in a microbiologically stable form. Microbiological stability can be achieved by any suitable means, such as by (i) freezing, refrigeration, or lyophilization of kit components, (ii) by heat-, chemical-, or filtration-mediated sterilization or partial sterilization, and/or (iii) by the addition of antimicrobial agents such as azide, detergents, and other suitable reagents to other kit components. The kit can also be optionally provided in a suitable housing that is preferably useful for robotic handling by a clinically-useful sample analyzer. For example, the kit can optionally comprise multiple liquids, each of which are stored in distinct compartments within the housing. In turn, each compartment can be sealed by a device that can be removed, or easily penetrated, by a mechanical device.

The following examples merely illustrate the best mode now contemplated for practicing the invention, but should not be construed to limit the invention. All literature citations herein are expressly incorporated by reference.

EXAMPLE 1

This example describes the identification of the H101Y missense mutation in the protein kinase C gamma gene and demonstrates that this mutation co-segregates with ataxic neurological disease.

<u>Mapping an autosomal dominant cerebellar ataxia to Chromosome 19q13.4-qter</u>: A four generation family of English and Dutch ethnic background with 14 family members exhibiting unexplained cerebellar ataxia was identified and designated AT08. See Brkanac et al., *Arch. Neurol.* Vol. 59 (Aug. 2002). The family has a relatively uncomplicated form of cerebellar ataxia with mean age of onset of 33 years (range 10 to 50 years) with no evidence for a shortened lifespan and without any differentiating features (such as cognitive decline, visual or other sensory loss, axial myoclonus or peripheral neuropathy). Blood samples were obtained from 24 members in 2 generations of family AT08. DNA was extracted from leukocytes or Epstein-Barr virus-transformed B-lymphoblastoid cell lines as described in Raskind et al., *Am. J. Hum. Genet. 56*:1132-1139 (1995). To identify the locus responsible for the phenotype in this family, a whole genome linkage analysis was performed at the 10 centimorgan (cM) level using the methods as described in Brkanac, Z., et al., *Am. J. Med. Genet. 114*:450-457 (2002). One

primer of each pair was end-labeled with gamma 32 phosphorus by a T4 kinase reaction. By haplotype construction, a 22 cM critical region in band 19q13.4 to the q telomere cosegregating with the disease was defined with all the affected individuals found to carry the disease-associated haplotype (see Brkanac et al., *Arch. Neurol.* Vol. 59, 2002)).

Identification of PRKCG gene mutations: Based on sequence data available as of June 2002, a query of the NCBI database disclosed more than 300 genes that mapped to the critical region identified on chromosome 19q (see Brkanac et al., *Arch. Neurol.* Vol. 59, 2002)). PRKCG was identified as a gene that mapped to the critical region on chromosome 19q and was evaluated for DNA sequence alterations in family AT08.

PCR Amplification of Exons 1-18: DNA was isolated from peripheral blood and each of the 18 exons of the PRKCG gene were PCR-amplified from subject genomic DNA utilizing primer pairs listed in TABLE 1 and TABLE 2. PCR reactions were carried out in 20 µl containing 1X PCR buffer of 10 mM Tris-HCL (pH 8.3 at 25°C), 50 mM KCL, 1.5 mM $MgCl^2$, 0.001% (w/v) gelatin at final concentration, 10 pmol of each forward and reverse primer, 200 µM dNTP (Sigma, St. Louis, MO), and 1.0U JumpStart Taq DNA Polymerase (Sigma, St. Louis, MO). The PCR amplification protocol included an initial denaturation at 95°C for 5 min., 34 cycles of 94°C for 30 sec., 60°C (or 56°C for some fragments listed in TABLE 2) for 45 sec. and 72°C for 90 sec., followed by a final extension at 72°C for 10 min. 5 µl of PCR product was characterized by gel electrophoresis/ethidium bromide staining for the presence of a single correctly sized band.

Direct DNA sequencing of the PCR Fragments: 5 µl of PCR product from each sample confirmed to have a single correctly sized band was treated with 1 µl of ExoSAP-IT (US Biochemical, Cleveland, OH) at 37°C for 2 hours followed by heat inactivation at 85°C for 10 minutes. Direct DNA sequencing of the purified fragments was carried out by using a BigDye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems Inc., Foster City, CA). The primers used for sequencing are listed in TABLE 2. For initial mutation screening, either forward or reverse primer was used. The PCR reaction contained 3 µl of treated PCR product (~100ng), 3 pmol primer, 1 µl sequencing buffer and 2 µl of BigDye reagent in a total volume of 10 µl. The sequencing reaction was carried out in a PTC-100 Programmable Thermal Controller (MJ Research Inc., Waltham, MA) with cycle conditions of 96°C for 2 min., 30 cycles of 96°C for

15 sec., 50°C for 10 sec. and 60°C for 4 min. The sequencing product was purified by ethanol/EDTA precipitation, then electrophoresed on an ABI DNA Sequencer (Applied Biosystems Inc., Foster City, CA).

Evaluation of cosegregation of ataxia and genetic mutations: Radioisotope dideoxy sequencing using two bases (wild type C and mutant T) was performed to evaluate the cosegregation of ataxia and the mutations in AT08 and to screen normal controls for a possible polymorphism. The forward primer for exon 4 was end-labeled with $[\gamma^{32}]P$ by the T4 kinase reaction and sequencing was performed with the AmpliCycle Sequencing Kit (Applied Biosytems Inc.). The sequencing products were then electrophoresed at 50°C on 6% polyacrylamide gels containing 7M urea.

Results:

The C to T transition in nucleotide 301 (H101Y) A C to T transition in nucleotide 301, (as counted from the cDNA start codon as shown in SEQ ID NO:1) was detected in exon 4, which predicts substitution of hydrophilic tyrosine for hydrophobic histidine at amino acid position 101 (H101Y). The mutation was found in 10 members of the family and segregated with ataxia in all ten cases. Of the group that is currently unaffected but at risk (twenty and younger), two individuals inherited the C to T mutation, and 13 individuals had the wild-type sequence. The C to T nucleotide change was not found in 192 normal controls (384 chromosomes). The 101 histidine residue in the Cys2 region is evolutionarily conserved in all mammals and invertebrates studied and in all Cys2 regions in the PRKCG family.

EXAMPLE 2

This example describes the identification of the S119P and G128D missense mutations in the protein kinase C gamma gene.

Subjects tested: Forty ataxia subjects were screened for mutations in the PRKCG gene. Twenty-seven of the subjects had positive family histories of ataxia, and twelve were sporadic cases. All forty subjects had previously tested negative for expansions in the genes for SCA1, SCA2, SCA3 and SCA6. Twenty-seven subjects had also tested negative for abnormal alleles of SCA7 and SCA8. Ninety-six control samples (192 chromosomes) were tested in this study.

Methods: The entire coding region of PRKCG was sequenced in genomic DNA by first PCR amplifying the 18 exons and sequencing each using the primers shown in TABLE 2 as described in Example 1.

Results:

T to C transition in nucleotide 355 (S119P): A T to C transition in nucleotide 355, predicting a hydrophilic serine to hydrophobic proline substitution at residue 119 (S119P) was found in an affected woman and her affected son and affected daughter (mean age of onset at 42 years, range 35 to 51 years; family AT29). Serine residue 119 is conserved in all mammalian cys2 regions and most PRKCG family members.

G to A transition in nucleotide 383 (G128D): A G to A transition in nucleotide 383 predicting a glycine to aspartate substitution at residue 128 (G128D) was found in a 55-year-old man (with onset of ataxia in his early twenties), with no family history of ataxia (family AT117). Glycine residue 128 is conserved in all mammalian cys2 regions and most PRKCG family members.

Controls: Of the ninety-six control samples (192 chromosomes) that were tested in this study, none exhibited either of these two single nucleotide changes.

EXAMPLE 3

This example describes the use of restriction fragment length polymorphism (RFLP) analysis to identify mutations in the PRKCG gene.

Restriction Fragment Length Polymorphism (RFLP) Analysis: Several of the identified mutations, including C69C, V68V, S119P, G128D, S361G, E561E and R597S, alter the restriction endonuclease digestion pattern of specific restriction endonucleases as shown in TABLE 4. The first column of TABLE 4 describes the mutations amenable to RFLP analysis, the second column provides a useful primer set for amplification of the region encompassing the mutation, the third column provides the relevant restriction endonuclease for use in digestion of the PCR fragment, the fourth and fifth columns provide the expected restriction enzyme digested fragments for wild-type, and mutant genes respectively. The final two columns provide the reaction conditions appropriate for each restriction enzyme digestion listed.

Results:

RFLP analysis was performed on samples from subjects exhibiting ataxia containing the S119P mutation and a panel of 96 normal control individuals. HaeIII digestion of the 260 bp exon 4 fragment from ataxia samples resulted in the pattern shown in TABLE 4 for mutant-type samples. Of the 96 normal control samples, all HaeIII restriction patterns corresponded to the expected fragment pattern for wild type shown in TABLE 4.

RFLP analysis was also performed on samples from subjects exhibiting ataxia containing the G128D mutation a panel of 96 normal control individuals. MwoI digestion of the 260 bp exon 4 fragment from ataxia samples resulted in the pattern shown in TABLE 4 for mutant-type samples. Of the 96 normal control samples, all MwoI restriction patterns corresponded to the expected fragment pattern for wild type shown in TABLE 4.

TABLE 4

THE CONDITIONS OF RFLP ANALYSIS FOR SCREEN IDENTIFIED MUTATIONS IN *PRKCG* GENE

Mutation	**Primer Set**	**Enzyme**	**Restriction Fragment Sizes (bp)**		**Conditions**	
			Wild-type	*Mutant-type*	*Temp*	*Buffer(s)*
207C to T (C69C)	3F (SEQ ID NO: 8), 3R (SEQ ID NO: 9)	PstI	95,156	251	37°C	NEBuffer 3 + BSA
204C to G (V68V)	3F (SEQ ID NO: 8), 3R (SEQ ID NO: 9)	BsgI	251	96,155	37°C	NEBuffer 4 + SAM
355T to C (S119P)	4F (SEQ ID NO: 10), 4R (SEQ ID NO: 11)	HaeIII	11,25,36,188	11,25,36,58,130	37°C	NEBuffer 2
383G to A (G128D)	4F (SEQ ID NO: 10), 4R (SEQ ID NO: 11)	MwoI	55,59,72,74	55,59,146	60°C	NEBuffer MwoI
1081A to G (S361G)	10F (SEQ ID NO: 20), 10R (SEQ ID NO: 21)	AciI	6,71,200	6,66,71,134	37°C	NEBuffer 3
1683G to A (E561E)	16F (SEQ ID NO: 30), 16R (SEQ ID NO: 31)	SapI	420	174,276	37°C	NEBuffer 4
1789C to A (R597S)	17F (SEQ ID NO: 32), 17R (SEQ ID NO: 33)	HaeII	94,176	270	37°C	NEBuffer 4 + BSA

EXAMPLE 4

This example describes a kit and method of use for identifying genetic mutations associated with ataxic neurological disease in a mammalian subject, and for determining susceptibility or presence of ataxic neurological disease in a test subject. Additional mutants R41P, S361G and R597S have been identified through the use of this kit and method.

Methods Utilized:

PCR Amplification: Carried out as described in Example 1

Direct Sequencing: Carried out as described in Example 1

Data Analysis: The resulting sequences were aligned with the known exon sequence using a multiple sequence alignment tool, Sequencher (Gene Codes Corporation, Ann Arbor, MI), in order to identify any nucleotide changes. Electropherograms were also visually examined to detect heterozygous base changes that might have been missed by Sequencher.

Confirmation of the Nucleotide Changes: Once a nucleotide change was detected, the exon fragment encompassing the suspected mutation was subjected to PCR amplification and direct sequencing again, using both forward and reverse primers.

For familial cases, when the nucleotide change is confirmed, with consent, the available family members, including affected and at risk unaffected individuals, are tested to confirm that the mutation segregates with the disease. After appropriate consent for clinical testing is obtained, the test may also be used for presymptomatic diagnosis in at-risk individuals.

Contents of the PRKCG Mutation Kit:

1. 10X PCR buffer (100 mM Tris-HCl (pH 8.3 at 25°C), 500 mM KCl, 15 mM $MgCl_2$, 0.01% (w/v) gelatin

2. dNTP mix: dATP, dCTP, dGTP, dTTP at 10 mM each (Sigma, St. Louis, MO)

3. JumpStart Taq DNA polymerase (Sigma, St. Louis, MO)

4. Primers for amplification of each PRKCG exon and the adjacent intronic sequences at 10 μM each (as shown in TABLE 1 and TABLE 2)

5. Exo-SAP-IT (US Biochemical, Cleveland, OH)

6. BigDye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems Inc., Foster City, CA)

Results:

A total of 160 individuals exhibiting ataxia were screened for mutations and the R41P, S361G and R597S mutations were found once each.

A G to C transition was discovered in nucleotide 122 predicting a R to P substitution at residue 41 in exon 1. An A to G transition was discovered in nucleotide 380 predicting a Q to R substitution at residue 127 in exon 4. An A to G transition was discovered in nucleotide 1081, predicting an S to G substitution at residue 361 in exon 10, and a C to A transition was discovered in nucleotide 1789 predicting an R to S substitution at residue 597 in exon 17.

While the preferred embodiment of the invention has been illustrated and described, it will be appreciated that various changes can be made therein without departing from the spirit and scope of the invention.